

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	18250	(530/350).CCLS.	US-PGPUB; USPAT; DERWENT	OR	OFF	2006/03/02 15:44
L2	0	L1 and "c-Cbl associated protein"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:44
L3	0	L1 and "Cbl associated protein"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:45
L4	2227	L1 and "CAP"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:45
L6	1098	L4 and insulin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:46
L7	27197	Oda.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:46
L8	395	L7 and CAP	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:47
L9	4	L8 and insulin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:46
L10	5466	CAP with (binding protein)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:47
L11	264	"CAP binding protein"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:47
L12	78	L11 and insulin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/03/02 15:47

# Untitled

db	242		GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGCTCCCGCGACCCCGACGTCC	301
qy	102		SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
db	302		TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
qy	122		GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
db	362		CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
qy	142		LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
db	422		CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA	481
qy	162		AlaAspLeuHisIlePheAspCys	169
db	482		GCAGACTTGCATATATTTGACTGC	505

# Untitled

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1097)  
 AUTHORS Cronshaw,J.M., Krutchinsky,A.N., Zhang,W., Chait,B.T. and  
 Matunis,M.J.  
 TITLE Proteomic analysis of the mammalian nuclear pore complex  
 JOURNAL J. Cell Biol. 158 (5), 915-927 (2002)  
 PUBMED 12196509  
 REFERENCE 2 (bases 1 to 1097)  
 AUTHORS Cronshaw,J.M. and Matunis,M.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAY-2002) Biochemistry and Molecular Biology, Johns  
 Hopkins Bloomberg School of Public Health, 615 N. Wolfe St.,  
 Baltimore, MD 21205, USA  
 FEATURES  
 source Location/Qualifiers  
 1. .1097  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3936128"  
 CDS  
 <1. .817  
 /note="enriched at the nuclear periphery"  
 /codon\_start=2  
 /product="nuclear protein p30"  
 /protein\_id="AAM76703.1"  
 /db\_xref="GI:21717632"  
 /translation="RRSRSSAAAKLRGQKRS GASAAPAASAAAALAPSATRRRSASQ  
 AGSKSQAVEKPPSEK PRLRRSSPRAQEEGPEPPPELALLPPPPPPPTPATPTSSA  
 SNLDLGEQERWETFQKRQKLTSEGA AKLLLDTFEYQGLVKHTGGCHCGAVRFEVWAS  
 ADLHIFDCNCSICKKKQNRHFIVPASRFKLLKGAEHITTYTFNTHKAQHTFCKRCGVQ  
 SFYTPRSNPGGFGIAPHCLDEGTVRSMVTEEFNGSDWEKAMKEHKTIKMSKE"

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	8	Gaps:	0

US-10-530-886-2 (1-175) x AF514992 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
Qy	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGACACGGCGC	121
Qy	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTGGAGAAGCCG	181
Qy	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCCGCGGGCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCT	241
Qy	82	GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer	101

# Untitled

#5

JOURNAL diseases  
Patent: WO 2005019258-A 4392 03-MAR-2005;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. 1097  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

US-10-530-886-2 (1-175) x CS043838 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
Qy	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCCCGCGGCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC	121
Qy	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCGGAGAAGCCG	181
Qy	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCCGCGGGCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCT	241
Qy	82	GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer	101
Db	242	GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGACTCCCGCGACCCCGACGTCC	301
Qy	102	SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
Db	302	TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
Qy	122	GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
Db	362	CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
Qy	142	LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
Db	422	CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA	481
Qy	162	AlaAspLeuHisIlePheAspCys	169
Db	482	GCAGACTTGCATATATTTGACTGC	505

RESULT 5  
AF514992  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

AF514992 1097 bp mRNA linear PRI 16-SEP-2002  
Homo sapiens nuclear protein p30 mRNA, partial cds.  
AF514992  
AF514992.1 GI:21717631

# Untitled

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

US-10-530-886-2 (1-175) x CS043836 (1-1097)

QY	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
QY	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC	121
QY	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCGCTCGGAGAAGCCG	181
QY	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCCCGGGGCCAGGAGGAGGGCCGGGGGAGCCGCCGCCGCT	241
QY	82	GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer	101
Db	242	GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGCGCTCCCGCGACCCGACGTCC	301
QY	102	SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
Db	302	TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
QY	122	GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
Db	362	CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
QY	142	LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
Db	422	CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA	481
QY	162	AlaAspLeuHisIlePheAspCys	169
Db	482	GCAGACTTGCATATATTTGACTGC	505

### RESULT 4

CS043838

#### LOCUS

CS043838 1097 bp DNA linear PAT 22-MAR-2005

#### DEFINITION

Sequence 4392 from Patent WO2005019258.

#### ACCESSION

CS043838

#### VERSION

CS043838.1 GI:61850673

#### KEYWORDS

#### SOURCE

Homo sapiens (human)

#### ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

#### REFERENCE

1

#### AUTHORS

Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.

#### TITLE

Compositions and methods for the treatment of immune related

DB: 6 Untitled  
Gaps: 0

US-10-530-886-2 (1-175) x CS034886 (1-1097)

```

Qy      2 ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer 21
        |||
Db      2 CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC 61

Qy     22 AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg 41
        |||
Db     62 GCGGCCCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGGCGC 121

Qy     42 SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro 61
        |||
Db    122 TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCCGAGAAGCCG 181

Qy     62 ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro 81
        |||
Db    182 CGGCTGAGGCGCTCGTCGCCCGGGCCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCT 241

Qy     82 GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer 101
        |||
Db    242 GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGCGCCGACTCCCGCGACCCCGACGTCC 301

Qy    102 SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg 121
        |||
Db    302 TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCCG 361

Qy    122 GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly 141
        |||
Db    362 CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC 421

Qy    142 LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer 161
        |||
Db    422 CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA 481

Qy    162 AlaAspLeuHisIlePheAspCys 169
        |||
Db    482 GCAGACTTGTCATATATTTGACTGC 505

```

RESULT 3  
CS043836

LOCUS CS043836 1097 bp DNA linear PAT 22-MAR-2005

DEFINITION Sequence 4390 from Patent WO2005019258.

ACCESSION CS043836

VERSION CS043836.1 GI:61850672

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

1  
Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.  
Compositions and methods for the treatment of immune related  
diseases

JOURNAL

Patent: WO 2005019258-A 4390 03-MAR-2005;  
Genentech, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1097

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Untitled

```

Qy      22  AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg  41
      |||
Db      62  GCGGCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC  121

Qy      42  SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro  61
      |||
Db     122  TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCGGAGAAGCCG  181

Qy      62  ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro  81
      |||
Db     182  CGGCTGAGGCGCTCGTCGCCGCGGGCCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCCT  241

Qy      82  GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer  101
      |||
Db     242  GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGACTCCCGCGACCCCGACGTCC  301

Qy     102  SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg  121
      |||
Db     302  TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG  361

Qy     122  GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly  141
      |||
Db     362  CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC  421

Qy     142  LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer  161
      |||
Db     422  CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA  481

Qy     162  AlaAspLeuHisIlePheAspCys  169
      |||
Db     482  GCAGACTTGCATATATTTGACTGC  505

```

# RESULT 2

CS034886 1097 bp DNA linear PAT 10-MAR-2005

LOCUS CS034886 Sequence 4392 from Patent WO2005016962.

ACCESSION CS034886

VERSION CS034886.1 GI:60733238

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1  
AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.  
TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 2005016962-A 4392 24-FEB-2005; Genentech, Inc. (US)

## FEATURES

source

Location/Qualifiers

1..1097

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0

				Untitled		
C	56	12	6.9	188633	9	AL606932
C	57	12	6.9	193411	14	BX813304
C	58	12	6.9	200568	14	AC093318
	59	12	6.9	201389	14	AC093358
C	60	12	6.9	202932	9	AC153890
	61	12	6.9	204134	9	AC145116
C	62	12	6.9	207105	14	AC123332
C	63	12	6.9	210145	5	CR387996
C	64	12	6.9	210969	9	AC139758
	65	12	6.9	216290	14	AC151275
	66	12	6.9	224054	14	AC097089
	67	12	6.9	230871	14	AC162361
C	68	12	6.9	230951	14	AC120683
	69	12	6.9	235703	9	AC113970
C	70	12	6.9	244853	14	AC103346
C	71	12	6.9	253961	14	AC128235
C	72	12	6.9	254581	14	AC111674
C	73	12	6.9	256496	9	AC158239
	74	12	6.9	265797	9	AC099884
	75	12	6.9	271069	14	AC127915

AL606932 Mouse DNA  
 BX813304 Danio rer  
 AC093318 Mus muscu  
 AC093358 Mus muscu  
 AC153890 Mus muscu  
 AC145116 Mus muscu  
 AC123332 Rattus no  
 CR387996 Zebrafish  
 AC139758 Mus muscu  
 AC151275 Mus muscu  
 AC097089 Rattus no  
 AC162361 Mus muscu  
 AC120683 Rattus no  
 AC113970 Mus muscu  
 AC103346 Rattus no  
 AC128235 Rattus no  
 AC111674 Rattus no  
 AC158239 Mus muscu  
 AC099884 Mus muscu  
 AC127915 Rattus no

# ALIGNMENTS

RESULT 1  
 CS034884  
 LOCUS CS034884 1097 bp DNA linear PAT 10-MAR-2005  
 DEFINITION Sequence 4390 from Patent WO2005016962.  
 ACCESSION CS034884  
 VERSION CS034884.1 GI:60733237  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.  
 TITLE Compositions and methods for the treatment of immune related  
 diseases  
 JOURNAL Patent: WO 2005016962-A 4390 24-FEB-2005;  
 Genentech, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. .1097  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

US-10-530-886-2 (1-175) x CS034884 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61



Untitled  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	168	96.0	1097	6	CS034884	CS034884 Sequence
2	168	96.0	1097	6	CS034886	CS034886 Sequence
3	168	96.0	1097	6	CS043836	CS043836 Sequence
4	168	96.0	1097	6	CS043838	CS043838 Sequence
5	168	96.0	1097	8	AF514992	AF514992 Homo sapi
6	152	86.9	1191	8	BC052604	BC052604 Homo sapi
7	136	77.7	161943	8	HS84M10	AL356460 Homo sapi
8	136	77.7	192307	8	AC005971	AC005971 Homo sapi
c 9	119	68.0	170944	8	AC093484	AC093484 Homo sapi
10	109	62.3	926	8	HSA332538	AJ332538 Homo sapi
11	84	48.0	1797	6	CS036951	CS036951 Sequence
12	84	48.0	1797	6	CS045903	CS045903 Sequence
13	72	41.1	1005	6	AR447632	AR447632 Sequence
14	50	28.6	579	6	CQ724012	CQ724012 Sequence
15	45	25.7	723	8	HSA330089	AJ330089 Homo sapi
c 16	33	18.9	181719	14	AL662863	AL662863 Mus muscu
17	33	18.9	195339	9	AL596181	AL596181 Mouse DNA
18	33	18.9	322497	14	AC112109	AC112109 Rattus no
19	30	17.1	300	6	BD220196	BD220196 Human gen
20	27	15.4	147951	14	AC143662	AC143662 Macaca mu
c 21	19	10.9	193129	5	AL953908	AL953908 Zebrafish
22	19	10.9	206722	5	CR848813	CR848813 Zebrafish
c 23	17	9.7	2602	2	AK112512	AK112512 Ciona int
24	13	7.4	572	5	CR389739	CR389739 Gallus ga
25	13	7.4	744	5	CR352613	CR352613 Gallus ga
26	13	7.4	110001	14	AC151687	AC151687 Gallus ga
27	13	7.4	349142	1	BX572599	BX572599 Rhodopseu
c 28	12	6.9	224	15	AY022843	AY022843 Oryza sat
c 29	12	6.9	560	10	BV223329	BV223329 S233P6545
30	12	6.9	644	15	AY429384	AY429384 Arabidops
31	12	6.9	741	15	AF345338	AF345338 Arabidops
32	12	6.9	911	15	AF447888	AF447888 Arabidops
33	12	6.9	1203	15	AB091677	AB091677 Periploca
34	12	6.9	2100	15	AB071299	AB071299 Oryza sat
35	12	6.9	2510	5	BC098960	BC098960 Xenopus l
36	12	6.9	3026	15	AK100322	AK100322 Oryza sat
37	12	6.9	6297	9	AF227194	AF227194 Mus muscu
c 38	12	6.9	62850	14	AC100009	AC100009 Mus muscu
39	12	6.9	63451	8	AL662886	AL662886 Human DNA
c 40	12	6.9	79272	15	AC002338	AC002338 Arabidops
41	12	6.9	110000	15	AP008212_281	Continuation (282
42	12	6.9	110000	15	AP008212_282	Continuation (283
43	12	6.9	135378	8	AL390060	AL390060 Human DNA
44	12	6.9	143589	9	AC124745	AC124745 Mus muscu
45	12	6.9	147009	14	AC084179	AC084179 Homo sapi
46	12	6.9	150502	9	AC127563	AC127563 Mus muscu
47	12	6.9	156517	15	AP005395	AP005395 Oryza sat
48	12	6.9	157110	8	AL929101	AL929101 Human DNA
49	12	6.9	160562	9	AC164299	AC164299 Mus muscu
50	12	6.9	161012	14	AP004277	AP004277 Oryza sat
c 51	12	6.9	170871	14	AC084135	AC084135 Homo sapi
52	12	6.9	175754	15	AP003766	AP003766 Oryza sat
53	12	6.9	182841	5	BX248326	BX248326 Zebrafish
54	12	6.9	185174	9	AC136004	AC136004 Mus muscu
55	12	6.9	185321	8	AC123908	AC123908 Homo sapi

Untitled

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

Result #5

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 00:57:07 ; Search time 3092 seconds  
(without alignments)  
3217.210 Million cell updates/sec

Title: US-10-530-886-2  
Perfect score: 175  
Sequence: 1 MRRSRSSAAAKLRGQKRSGA.....FEVWASADLHIFDCKYRNYI 175

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11757827

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10530886/runat\_12012006\_070942\_6072/app\_query.fasta\_1.654

-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=75  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10530886\_@CGN\_1\_1\_7724\_@runat\_12012006\_070942\_6072 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a

# Untitled

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RA Director MGC Project;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC052604; AAH52604.1; -; mRNA.  
 DR Ensembl; ENSG00000166582; Homo sapiens.  
 DR HGNC; HGNC:29920; PRR6.  
 DR GO; GO:0016846; F:carbon-sulfur lyase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR006913; GFA.  
 DR Pfam; PF04828; DUF636; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 275 AA; 29946 MW; E9A69F1F9BA746D8 CRC64;

Query Match 96.6%; Score 172; DB 2; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-141;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRSRSSAAAKLRGQKRSGASGASAAPAASAAAALAPSATRTRRSASQAGSKSQAVEKPP 60  
 |||||  
 Db 1 MRRSRSSAAAKLRGQKRSGASGASAAPAASAAAALAPSATRTRRSASQAGSKSQAVEKPP 60  
 QY 61 SEKPLRRSSPRAQEEGPGEPPPELALLPPPPPPPTPATPTSSASNLDLGEQRRWET 120  
 |||||  
 Db 61 SEKPLRRSSPRAQEEGPGEPPPELALLPPPPPPPTPATPTSSASNLDLGEQRRWET 120  
 QY 121 FQKRQKLTSEGAAKLLLDTFEYQGLVKHTGGCHCGAVRFEVWASADLHIFDC 172  
 |||||  
 Db 121 FQKRQKLTSEGAAKLLLDTFEYQGLVKHTGGCHCGAVRFEVWASADLHIFDC 172

Untitled							
30	10	5.6	225	2	Q84NL2_ORYSA	Q84n12	oryza sativ
31	10	5.6	230	2	Q7XV57_ORYSA	Q7xv57	oryza sativ
32	10	5.6	230	2	Q84275_HPV47	Q84275	human papil
33	10	5.6	232	1	ACROL_HUMAN	P58840	homo sapien
34	10	5.6	266	2	Q52MA4_XENTR	Q52ma4	xenopus tro
35	10	5.6	273	2	Q5ZBY8_ORYSA	Q5zby8	oryza sativ
36	10	5.6	279	2	Q5C8Q0_9ADEN	Q5c8q0	simian aden
37	10	5.6	282	2	Q8BRU0_MOUSE	Q8bru0	mus musculu
38	10	5.6	283	2	Q6EPA2_ORYSA	Q6epa2	oryza sativ
39	10	5.6	294	2	Q8N144_HUMAN	Q8n144	homo sapien
40	10	5.6	300	2	Q4THH6_TETNG	Q4thh6	tetraodon n
41	10	5.6	304	1	VE4_HPV47	P22421	human papil
42	10	5.6	318	2	Q53JG2_ORYSA	Q53jg2	oryza sativ
43	10	5.6	331	2	Q6P0G2_BRARE	Q6p0g2	brachydanio
44	10	5.6	356	2	Q8LIR8_ORYSA	Q8lir8	oryza sativ
45	10	5.6	373	1	FBLI1_HUMAN	Q8wup2	homo sapien
46	10	5.6	396	2	Q6NTF6_HUMAN	Q6ntf6	homo sapien
47	10	5.6	398	1	SP5_MOUSE	Q9jhx2	mus musculu
48	10	5.6	398	2	Q6BEB4_HUMAN	Q6beb4	homo sapien
49	10	5.6	412	2	Q5CAF6_ORYSA	Q5caf6	oryza sativ
50	10	5.6	421	1	ACRO_HUMAN	P10323	homo sapien
51	10	5.6	421	2	Q6ICK2_HUMAN	Q6ick2	homo sapien
52	10	5.6	427	2	Q6ETL2_ORYSA	Q6etl2	oryza sativ
53	10	5.6	457	2	Q52KK4_RAT	Q52kk4	rattus norv
54	10	5.6	461	2	Q5BJ21_BRARE	Q5bj21	brachydanio
55	10	5.6	468	2	Q6P941_BRARE	Q6p941	brachydanio
56	10	5.6	472	2	Q5U4A3_XENLA	Q5u4a3	xenopus lae
57	10	5.6	476	2	Q9SCT7_ARATH	Q9sct7	arabidopsis
58	10	5.6	476	2	Q5ZKA6_CHICK	Q5zka6	gallus gall
59	10	5.6	478	2	Q51TL5_MAGGR	Q51tl5	magnaporthe
60	10	5.6	489	2	Q86XT7_HUMAN	Q86xt7	homo sapien
61	10	5.6	495	2	Q6C8G0_YARLI	Q6c8g0	yarrowia li
62	10	5.6	497	2	Q54LW2_DICDI	Q54lw2	dictyosteli
63	10	5.6	519	2	Q48655_ORYSA	Q48655	oryza sativ
64	10	5.6	545	2	Q6YS18_ORYSA	Q6ys18	oryza sativ
65	10	5.6	585	2	Q6RJN6_PHYPA	Q6rjn6	physcomitre
66	10	5.6	592	2	Q6RJN7_PHYPA	Q6rjn7	physcomitre
67	10	5.6	618	2	Q8S6K9_ORYSA	Q8s6k9	oryza sativ
68	10	5.6	618	2	Q99KV8_MOUSE	Q99kv8	mus musculu
69	10	5.6	666	2	Q7TVG2_MYCBO	Q7tvq2	mycobacteri
70	10	5.6	666	2	Q69740_MYCTU	Q69740	mycobacteri
71	10	5.6	670	2	Q8RVE5_ORYSA	Q8rve5	oryza sativ
72	10	5.6	670	2	Q593S5_CYPCA	Q593s5	cyprinus ca
73	10	5.6	672	2	Q8LMH2_ORYSA	Q8lmh2	oryza sativ
74	10	5.6	687	2	Q8BKD3_MOUSE	Q8bkd3	mus musculu
75	10	5.6	698	2	Q7XF73_ORYSA	Q7xf73	oryza sativ

# ALIGNMENTS

## RESULT 1

Q7Z7K6\_HUMAN

ID Q7Z7K6\_HUMAN PRELIMINARY; PRT; 275 AA.

AC Q7Z7K6;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PRR6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Blood;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

# Untitled

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

Result # 1

OM protein - protein search, using sw model

Run on: January 12, 2006, 12:44:40 ; Search time 116.986 Seconds  
(without alignments)  
1073.498 Million cell updates/sec

Title: US-10-530-886-4  
Perfect score: 178  
Sequence: 1 MRRSRSSAAAKLRGQKRSGA.....FEVWASADLHIFDCKYRNYI 178

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	96.6	275	2	Q7Z7K6_HUMAN	Q7z7k6 homo sapien
2	152	85.4	271	2	Q8NFH6_HUMAN	Q8nfh6 homo sapien
3	43	24.2	252	2	Q5SX21_MOUSE	Q5sx21 mus musculu
4	43	24.2	252	2	Q9CXS4_MOUSE	Q9cxs4 mus musculu
5	17	9.6	569	2	Q4SLH6_TETNG	Q4slh6 tetraodon n
6	13	7.3	141	2	Q6N8J6_RHOPA	Q6n8j6 rhodopseudo
7	12	6.7	268	1	LBD13_ARATH	Q9at61 arabidopsis
8	12	6.7	365	2	Q4KLX2_XENLA	Q4klx2 xenopus lae
9	12	6.7	700	2	Q8S976_ORYSA	Q8s976 oryza sativ
10	12	6.7	700	2	Q653H7_ORYSA	Q653h7 oryza sativ
11	12	6.7	2025	2	Q99PP2_MOUSE	Q99pp2 mus musculu
12	11	6.2	136	2	Q9CVJ1_MOUSE	Q9cvj1 mus musculu
13	11	6.2	301	2	Q6L4D1_ORYSA	Q6l4d1 oryza sativ
14	11	6.2	425	2	Q8ND23_HUMAN	Q8nd23 homo sapien
15	11	6.2	588	2	Q5XHY1_RAT	Q5xhy1 rattus norv
16	11	6.2	613	2	Q6ZLD1_ORYSA	Q6zld1 oryza sativ
17	10	5.6	65	2	Q8QTC1_WSSV	Q8qtc1 white spot
18	10	5.6	65	2	Q8VAQ0_WSSV	Q8vaq0 white spot
19	10	5.6	74	2	Q59EF8_HUMAN	Q59ef8 homo sapien
20	10	5.6	130	2	Q4J1V7_AZOVI	Q4j1v7 azotobacter
21	10	5.6	134	2	Q5DGR5_SCHJA	Q5dgr5 schistosoma
22	10	5.6	137	2	Q69U86_ORYSA	Q69u86 oryza sativ
23	10	5.6	137	2	Q4JMU1_9BACT	Q4jmu1 uncultured
24	10	5.6	137	2	Q7NFC1_GLOVI	Q7nfc1 gloeobacter
25	10	5.6	138	2	Q7QE51_ANOGA	Q7qe51 anopheles g
26	10	5.6	151	1	YWIS_WHEAT	P14723 triticum ae
27	10	5.6	158	2	Q9DVW0_9BACU	Q9dvw0 plutella xy
28	10	5.6	185	1	NO20_SOYBN	P08960 glycine max
29	10	5.6	221	2	O49946_SOLTU	O49946 solanum tub

Untitled

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

*Result #5*

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 00:57:07 ; Search time 3092 Seconds  
(without alignments)  
3217.210 Million cell updates/sec

Title: US-10-530-886-2  
Perfect score: 175  
Sequence: 1 MRRSRSSAAAKLRGQKRSGA.....FEVWASADLHIFDCKYRNYI 175

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11757827

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10530886/runat\_12012006\_070942\_6072/app\_query.fasta\_1.654

-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=75  
-DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10530886\_@CGN\_1\_1\_7724\_@runat\_12012006\_070942\_6072 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a

Untitled  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	168	96.0	1097	6	CS034884	CS034884 Sequence
2	168	96.0	1097	6	CS034886	CS034886 Sequence
3	168	96.0	1097	6	CS043836	CS043836 Sequence
4	168	96.0	1097	6	CS043838	CS043838 Sequence
5	168	96.0	1097	8	AF514992	AF514992 Homo sapi
6	152	86.9	1191	8	BC052604	BC052604 Homo sapi
7	136	77.7	161943	8	HS84M10	AL356460 Homo sapi
8	136	77.7	192307	8	AC005971	AC005971 Homo sapi
c 9	119	68.0	170944	8	AC093484	AC093484 Homo sapi
10	109	62.3	926	8	HSA332538	AJ332538 Homo sapi
11	84	48.0	1797	6	CS036951	CS036951 Sequence
12	84	48.0	1797	6	CS045903	CS045903 Sequence
13	72	41.1	1005	6	AR447632	AR447632 Sequence
14	50	28.6	579	6	CQ724012	CQ724012 Sequence
15	45	25.7	723	8	HSA330089	AJ330089 Homo sapi
c 16	33	18.9	181719	14	AL662863	AL662863 Mus muscu
17	33	18.9	195339	9	AL596181	AL596181 Mouse DNA
18	33	18.9	322497	14	AC112109	AC112109 Rattus no
19	30	17.1	300	6	BD220196	BD220196 Human gen
20	27	15.4	147951	14	AC143662	AC143662 Macaca mu
c 21	19	10.9	193129	5	AL953908	AL953908 Zebrafish
22	19	10.9	206722	5	CR848813	CR848813 Zebrafish
c 23	17	9.7	2602	2	AK112512	AK112512 Ciona int
24	13	7.4	572	5	CR389739	CR389739 Gallus ga
25	13	7.4	744	5	CR352613	CR352613 Gallus ga
26	13	7.4	110001	14	AC151687	AC151687 Gallus ga
27	13	7.4	349142	1	BX572599	BX572599 Rhodopseu
c 28	12	6.9	224	15	AY022843	AY022843 Oryza sat
c 29	12	6.9	560	10	BV223329	BV223329 S233P6545
30	12	6.9	644	15	AY429384	AY429384 Arabidops
31	12	6.9	741	15	AF345338	AF345338 Arabidops
32	12	6.9	911	15	AF447888	AF447888 Arabidops
33	12	6.9	1203	15	AB091677	AB091677 Periploca
34	12	6.9	2100	15	AB071299	AB071299 Oryza sat
35	12	6.9	2510	5	BC098960	BC098960 Xenopus l
36	12	6.9	3026	15	AK100322	AK100322 Oryza sat
37	12	6.9	6297	9	AF227194	AF227194 Mus muscu
c 38	12	6.9	62850	14	AC100009	AC100009 Mus muscu
39	12	6.9	63451	8	AL662886	AL662886 Human DNA
c 40	12	6.9	79272	15	AC002338	AC002338 Arabidops
41	12	6.9	110000	15	AP008212_281	Continuation (282
42	12	6.9	110000	15	AP008212_282	Continuation (283
43	12	6.9	135378	8	AL390060	AL390060 Human DNA
44	12	6.9	143589	9	AC124745	AC124745 Mus muscu
45	12	6.9	147009	14	AC084179	AC084179 Homo sapi
46	12	6.9	150502	9	AC127563	AC127563 Mus muscu
47	12	6.9	156517	15	AP005395	AP005395 Oryza sat
48	12	6.9	157110	8	AL929101	AL929101 Human DNA
49	12	6.9	160562	9	AC164299	AC164299 Mus muscu
50	12	6.9	161012	14	AP004277	AP004277 Oryza sat
c 51	12	6.9	170871	14	AC084135	AC084135 Homo sapi
52	12	6.9	175754	15	AP003766	AP003766 Oryza sat
53	12	6.9	182841	5	BX248326	BX248326 Zebrafish
54	12	6.9	185174	9	AC136004	AC136004 Mus muscu
55	12	6.9	185321	8	AC123908	AC123908 Homo sapi

					Untitled		
c	56	12	6.9	188633	9	AL606932	AL606932 Mouse DNA
c	57	12	6.9	193411	14	BX813304	BX813304 Danio rer
c	58	12	6.9	200568	14	AC093318	AC093318 Mus muscu
	59	12	6.9	201389	14	AC093358	AC093358 Mus muscu
c	60	12	6.9	202932	9	AC153890	AC153890 Mus muscu
	61	12	6.9	204134	9	AC145116	AC145116 Mus muscu
c	62	12	6.9	207105	14	AC123332	AC123332 Rattus no
c	63	12	6.9	210145	5	CR387996	CR387996 Zebrafish
c	64	12	6.9	210969	9	AC139758	AC139758 Mus muscu
	65	12	6.9	216290	14	AC151275	AC151275 Mus muscu
	66	12	6.9	224054	14	AC097089	AC097089 Rattus no
	67	12	6.9	230871	14	AC162361	AC162361 Mus muscu
c	68	12	6.9	230951	14	AC120683	AC120683 Rattus no
	69	12	6.9	235703	9	AC113970	AC113970 Mus muscu
c	70	12	6.9	244853	14	AC103346	AC103346 Rattus no
c	71	12	6.9	253961	14	AC128235	AC128235 Rattus no
c	72	12	6.9	254581	14	AC111674	AC111674 Rattus no
c	73	12	6.9	256496	9	AC158239	AC158239 Mus muscu
	74	12	6.9	265797	9	AC099884	AC099884 Mus muscu
	75	12	6.9	271069	14	AC127915	AC127915 Rattus no

#### ALIGNMENTS

#### RESULT 1

CS034884

LOCUS CS034884 1097 bp DNA linear PAT 10-MAR-2005

DEFINITION Sequence 4390 from Patent WO2005016962.

ACCESSION CS034884

VERSION CS034884.1 GI:60733237

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

1 Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.

TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 2005016962-A 4390 24-FEB-2005;  
Genentech, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1097

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

US-10-530-886-2 (1-175) x CS034884 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61



Untitled

```

Qy      22 AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg 41
      |||
Db      62 GCGGCCCCCGCGGCCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC 121

Qy      42 SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro 61
      |||
Db     122 TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCGGAGAAGCCG 181

Qy      62 ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro 81
      |||
Db     182 CGGCTGAGGCGCTCGTCGCCGCGGGCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCT 241

Qy      82 GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer 101
      |||
Db     242 GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGACTCCCGCGACCCCGACGTCC 301

Qy     102 SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg 121
      |||
Db     302 TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG 361

Qy     122 GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly 141
      |||
Db     362 CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC 421

Qy     142 LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer 161
      |||
Db     422 CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTGGGCCTCA 481

Qy     162 AlaAspLeuHisIlePheAspCys 169
      |||
Db     482 GCAGACTTGCATATATTTGACTGC 505

```

# RESULT 2

CS034886

LOCUS CS034886 1097 bp DNA linear PAT 10-MAR-2005

DEFINITION Sequence 4392 from Patent WO2005016962.

ACCESSION CS034886

VERSION CS034886.1 GI:60733238

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.

TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 2005016962-A 4392 24-FEB-2005; Genentech, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1097

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0

DB: 6 Untitled  
Gaps: 0

US-10-530-886-2 (1-175) x CS034886 (1-1097)

```

Qy      2 ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer 21
      |||
Db      2 CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC 61

Qy     22 AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg 41
      |||
Db     62 GCGGCCCGCGGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC 121

Qy     42 SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro 61
      |||
Db    122 TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCGGAGAAGCCG 181

Qy     62 ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro 81
      |||
Db    182 CGGCTGAGGCGCTCGTCGCCGCGGGCCAGGAGGAGGGCCCGGGGAGCCGCCGCCGCT 241

Qy     82 GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer 101
      |||
Db    242 GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGCGACTCCCGCGACCCCGACGTCC 301

Qy    102 SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg 121
      |||
Db    302 TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG 361

Qy    122 GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly 141
      |||
Db    362 CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC 421

Qy    142 LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer 161
      |||
Db    422 CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA 481

Qy    162 AlaAspLeuHisIlePheAspCys 169
      |||
Db    482 GCAGACTTGCATATATTTGACTGC 505

```

# RESULT 3 CS043836

LOCUS CS043836 1097 bp DNA linear PAT 22-MAR-2005

DEFINITION Sequence 4390 from Patent WO2005019258.

ACCESSION CS043836

VERSION CS043836.1 GI:61850672

## KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1  
AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.  
TITLE Compositions and methods for the treatment of immune related  
diseases

JOURNAL Patent: WO 2005019258-A 4390 03-MAR-2005;  
Genentech, Inc. (US)

## FEATURES

source

Location/Qualifiers

1. .1097

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

# Untitled

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

US-10-530-886-2 (1-175) x CS043836 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
Qy	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCGCGGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC	121
Qy	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTGCGAGAAGCCG	181
Qy	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCGCGGGCCAGGAGGAGGGCCGGGGGAGCCGCCGCCGCT	241
Qy	82	GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer	101
Db	242	GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGACTCCCGCGACCCCGACGTCC	301
Qy	102	SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
Db	302	TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
Qy	122	GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
Db	362	CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
Qy	142	LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
Db	422	CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA	481
Qy	162	AlaAspLeuHisIlePheAspCys	169
Db	482	GCAGACTTGTCATATATTTGACTGC	505

## RESULT 4

CS043838

LOCUS

CS043838 1097 bp DNA linear PAT 22-MAR-2005

DEFINITION

Sequence 4392 from Patent WO2005019258.

ACCESSION

CS043838

VERSION

CS043838.1 GI:61850673

KEYWORDS

.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

AUTHORS

Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.

TITLE

Compositions and methods for the treatment of immune related

#5

## ORIGIN

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	6	Gaps:	0

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
Qy	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC	121
Qy	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCCGAGAAGCCG	181
Qy	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCCGCGGGGCCAGGAGGAGGGCCGGGGGAGCCGCCGCCGCCT	241
Qy	82	GluLeuAlaLeuLeuProProProProProProProProThrProAlaThrProThrSer	101
Db	242	GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCCGCGACTCCCGCGACCCCGACGTCC	301
Qy	102	SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
Db	302	TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
Qy	122	GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
Db	362	CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
Qy	142	LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
Db	422	CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCTTTTTGAAGTTTGGGCCTCA	481
Qy	162	AlaAspLeuHisIlePheAspCys	169
Db	482	GCAGACTTGCATATATTTGACTGC	505

AF514992 1097 bp mRNA linear PRI 16-SEP-2002  
Homo sapiens nuclear protein p30 mRNA, partial cds.  
AF514992  
AF514992.1 GI:21717631

# Untitled

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1097)  
 AUTHORS Cronshaw,J.M., Krutchinsky,A.N., Zhang,W., Chait,B.T. and  
 Matunis,M.J.  
 TITLE Proteomic analysis of the mammalian nuclear pore complex  
 JOURNAL J. Cell Biol. 158 (5), 915-927 (2002)  
 PUBMED 12196509  
 REFERENCE 2 (bases 1 to 1097)  
 AUTHORS Cronshaw,J.M. and Matunis,M.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAY-2002) Biochemistry and Molecular Biology, Johns  
 Hopkins Bloomberg School of Public Health, 615 N. Wolfe St.,  
 Baltimore, MD 21205, USA  
 FEATURES  
 source Location/Qualifiers  
 1. .1097  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3936128"  
 CDS  
 <1. .817  
 /note="enriched at the nuclear periphery"  
 /codon\_start=2  
 /product="nuclear protein p30"  
 /protein\_id="AAM76703.1"  
 /db\_xref="GI:21717632"  
 /translation="RRSRSSAAAKLRGQKRSAGASAAPAASAAAALAPSATRRRSASQ  
 AGSKSQAVEKPPSEKPRRLRRSPRAQEEGPGEPPELALLPPPPPPPTPATPTSSA  
 SNLDLGEQRERWETFKRQKLTSEGAAKLLLDTFEYQGLVKHTGGCHCGAVRFEVWAS  
 ADLHIFDCNCSICKKKQNRHFIVPASRFKLLKGAEHITTYTFNTHKAQHTFCKRCGVQ  
 SFYTPRSNPGGFGIAPHCLDEGTVRSMVTEEFNGSDWEKAMKEHKTIKNMSKE"

## ORIGIN

### Alignment Scores:

Pred. No.:	2.72e-142	Length:	1097
Score:	168.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.00%	Indels:	0
DB:	8	Gaps:	0

US-10-530-886-2 (1-175) x AF514992 (1-1097)

Qy	2	ArgArgSerArgSerSerAlaAlaAlaLysLeuArgGlyGlnLysArgSerGlyAlaSer	21
Db	2	CGGCGATCGAGGAGCTCTGCGGCCGCCAAGCTGCGCGGGCAGAAGCGGTCCGGGGCCTCC	61
Qy	22	AlaAlaProAlaAlaSerAlaAlaAlaAlaLeuAlaProSerAlaThrArgThrArgArg	41
Db	62	GCGGCCCCCGCGGCCTCCGCGGCCGCTGCCTTGGCACCCAGCGCCACCCGCACACGGCGC	121
Qy	42	SerAlaSerGlnAlaGlySerLysSerGlnAlaValGluLysProProSerGluLysPro	61
Db	122	TCCGCTAGCCAGGCCGGGAGCAAGAGCCAGGCGGTGGAGAAGCCGCCGTCGGAGAAGCCG	181
Qy	62	ArgLeuArgArgSerSerProArgAlaGlnGluGluGlyProGlyGluProProProPro	81
Db	182	CGGCTGAGGCGCTCGTCGCCGCGGGCCAGGAGGAGGGCCGGGGGAGCCGCCGCCGCT	241
Qy	82	GluLeuAlaLeuLeuProProProProProProProProProThrProAlaThrProThrSer	101

		Untitled	
Db	242	 GAGCTGGCGTTGCTCCCGCCACCGCCGCCGCCGCGCTCCCGCGACCCCGACGTCC	301
Qy	102	SerAlaSerAsnLeuAspLeuGlyGluGlnArgGluArgTrpGluThrPheGlnLysArg	121
Db	302	 TCGGCGTCCAACCTGGACCTGGGCGAGCAGCGGGAGCGCTGGGAGACGTTCCAGAAGCGG	361
Qy	122	GlnLysLeuThrSerGluGlyAlaAlaLysLeuLeuLeuAspThrPheGluTyrGlnGly	141
Db	362	 CAGAAGCTTACCTCCGAGGGTGCCGCCAAGCTCCTGCTAGACACCTTTGAATACCAGGGC	421
Qy	142	LeuValLysHisThrGlyGlyCysHisCysGlyAlaValArgPheGluValTrpAlaSer	161
Db	422	 CTGGTGAAGCACACAGGAGGCTGCCACTGTGGAGCAGTTCGTTTTGAAGTTTGGGCCTCA	481
Qy	162	AlaAspLeuHisIlePheAspCys	169
Db	482	 GCAGACTTGCATATATTTGACTGC	505

Untitled

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

Result #1

OM protein - protein search, using sw model

Run on: January 12, 2006, 12:44:40 ; Search time 116.986 Seconds  
(without alignments)  
1073.498 Million cell updates/sec

Title: US-10-530-886-4  
Perfect score: 178  
Sequence: 1 MRRSRSSAAAKLRGQKRSQA.....FEVWASADLHIFDCKYRNYI 178

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	96.6	275	2	Q7Z7K6_HUMAN	Q7z7k6 homo sapien
2	152	85.4	271	2	Q8NFH6_HUMAN	Q8nfh6 homo sapien
3	43	24.2	252	2	Q5SX21_MOUSE	Q5sx21 mus musculu
4	43	24.2	252	2	Q9CXS4_MOUSE	Q9cxs4 mus musculu
5	17	9.6	569	2	Q4SLH6_TETNG	Q4slh6 tetraodon n
6	13	7.3	141	2	Q6N8J6_RHOPA	Q6n8j6 rhodopseudo
7	12	6.7	268	1	LBD13_ARATH	Q9at61 arabidopsis
8	12	6.7	365	2	Q4KLX2_XENLA	Q4klx2 xenopus lae
9	12	6.7	700	2	Q8S976_ORYSA	Q8s976 oryza sativ
10	12	6.7	700	2	Q653H7_ORYSA	Q653h7 oryza sativ
11	12	6.7	2025	2	Q99PP2_MOUSE	Q99pp2 mus musculu
12	11	6.2	136	2	Q9CVJ1_MOUSE	Q9cvj1 mus musculu
13	11	6.2	301	2	Q6L4D1_ORYSA	Q6l4d1 oryza sativ
14	11	6.2	425	2	Q8ND23_HUMAN	Q8nd23 homo sapien
15	11	6.2	588	2	Q5XHY1_RAT	Q5xhy1 rattus norv
16	11	6.2	613	2	Q6ZLD1_ORYSA	Q6zld1 oryza sativ
17	10	5.6	65	2	Q8QTC1_WSSV	Q8qtc1 white spot
18	10	5.6	65	2	Q8VAQ0_WSSV	Q8vaq0 white spot
19	10	5.6	74	2	Q59EF8_HUMAN	Q59ef8 homo sapien
20	10	5.6	130	2	Q4J1V7_AZOVI	Q4j1v7 azotobacter
21	10	5.6	134	2	Q5DGR5_SCHJA	Q5dgr5 schistosoma
22	10	5.6	137	2	Q69U86_ORYSA	Q69u86 oryza sativ
23	10	5.6	137	2	Q4JMU1_9BACT	Q4jmu1 uncultured
24	10	5.6	137	2	Q7NFC1_GLOVI	Q7nfc1 gloebacter
25	10	5.6	138	2	Q7QE51_ANOGA	Q7qe51 anopheles g
26	10	5.6	151	1	YWIS_WHEAT	P14723 triticum ae
27	10	5.6	158	2	Q9DVW0_9BACU	Q9dvw0 plutella xy
28	10	5.6	185	1	NO20_SOYBN	P08960 glycine max
29	10	5.6	221	2	O49946_SOLTU	O49946 solanum tub

Untitled							
30	10	5.6	225	2	Q84NL2_ORYSA	Q84nl2	oryza sativ
31	10	5.6	230	2	Q7XV57_ORYSA	Q7xv57	oryza sativ
32	10	5.6	230	2	Q84275_HPV47	Q84275	human papil
33	10	5.6	232	1	ACROL_HUMAN	P58840	homo sapien
34	10	5.6	266	2	Q52MA4_XENTR	Q52ma4	xenopus tro
35	10	5.6	273	2	Q5ZBY8_ORYSA	Q5zby8	oryza sativ
36	10	5.6	279	2	Q5C8Q0_9ADEN	Q5c8q0	simian aden
37	10	5.6	282	2	Q8BRU0_MOUSE	Q8bru0	mus musculu
38	10	5.6	283	2	Q6EPA2_ORYSA	Q6epa2	oryza sativ
39	10	5.6	294	2	Q8N144_HUMAN	Q8n144	homo sapien
40	10	5.6	300	2	Q4THH6_TETNG	Q4thh6	tetraodon n
41	10	5.6	304	1	VE4_HPV47	P22421	human papil
42	10	5.6	318	2	Q53JG2_ORYSA	Q53jg2	oryza sativ
43	10	5.6	331	2	Q6P0G2_BRARE	Q6p0g2	brachydanio
44	10	5.6	356	2	Q8LIR8_ORYSA	Q8lir8	oryza sativ
45	10	5.6	373	1	FBLI1_HUMAN	Q8wup2	homo sapien
46	10	5.6	396	2	Q6NTF6_HUMAN	Q6ntf6	homo sapien
47	10	5.6	398	1	SP5_MOUSE	Q9jhx2	mus musculu
48	10	5.6	398	2	Q6BEB4_HUMAN	Q6beb4	homo sapien
49	10	5.6	412	2	Q5CAF6_ORYSA	Q5caf6	oryza sativ
50	10	5.6	421	1	ACRO_HUMAN	P10323	homo sapien
51	10	5.6	421	2	Q6ICK2_HUMAN	Q6ick2	homo sapien
52	10	5.6	427	2	Q6ETL2_ORYSA	Q6etl2	oryza sativ
53	10	5.6	457	2	Q52KK4_RAT	Q52kk4	rattus norv
54	10	5.6	461	2	Q5BJ21_BRARE	Q5bj21	brachydanio
55	10	5.6	468	2	Q6P941_BRARE	Q6p941	brachydanio
56	10	5.6	472	2	Q5U4A3_XENLA	Q5u4a3	xenopus lae
57	10	5.6	476	2	Q9SCT7_ARATH	Q9sct7	arabidopsis
58	10	5.6	476	2	Q5ZKA6_CHICK	Q5zka6	gallus gall
59	10	5.6	478	2	Q51TL5_MAGGR	Q51tl5	magnaporthe
60	10	5.6	489	2	Q86XT7_HUMAN	Q86xt7	homo sapien
61	10	5.6	495	2	Q6C8G0_YARLI	Q6c8g0	yarrowia li
62	10	5.6	497	2	Q54LW2_DICDI	Q54lw2	dictyosteli
63	10	5.6	519	2	O48655_ORYSA	O48655	oryza sativ
64	10	5.6	545	2	Q6YS18_ORYSA	Q6ys18	oryza sativ
65	10	5.6	585	2	Q6RJN6_PHYPA	Q6rjn6	physcomitre
66	10	5.6	592	2	Q6RJN7_PHYPA	Q6rjn7	physcomitre
67	10	5.6	618	2	Q8S6K9_ORYSA	Q8s6k9	oryza sativ
68	10	5.6	618	2	Q99KV8_MOUSE	Q99kv8	mus musculu
69	10	5.6	666	2	Q7TVG2_MYCBO	Q7tvq2	mycobacteri
70	10	5.6	666	2	O69740_MYCTU	O69740	mycobacteri
71	10	5.6	670	2	Q8RVE5_ORYSA	Q8rve5	oryza sativ
72	10	5.6	670	2	Q593S5_CYPCA	Q593s5	cyprinus ca
73	10	5.6	672	2	Q8LMH2_ORYSA	Q8lmh2	oryza sativ
74	10	5.6	687	2	Q8BKD3_MOUSE	Q8bkd3	mus musculu
75	10	5.6	698	2	Q7XF73_ORYSA	Q7xf73	oryza sativ

#### ALIGNMENTS

#### RESULT 1

Q7Z7K6\_HUMAN

ID Q7Z7K6\_HUMAN PRELIMINARY; PRT; 275 AA.

AC Q7Z7K6;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PRR6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Blood;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,



Untitled

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Blood;  
RA Director MGC Project;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC052604; AAH52604.1; -; mRNA.  
DR Ensembl; ENSG00000166582; Homo sapiens.  
DR HGNC; HGNC:29920; PRR6.  
DR GO; GO:0016846; F:carbon-sulfur lyase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR006913; GFA.  
DR Pfam; PF04828; DUF636; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 275 AA; 29946 MW; E9A69F1F9BA746D8 CRC64;

Query Match 96.6%; Score 172; DB 2; Length 275;  
Best Local Similarity 100.0%; Pred. No. 3.6e-141;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRSRSSAAAKLRGQKRSGASGASAAPASAAAALAPSATRTRRSASQAGSKSQAVEKPP	60
Db	1	MRRSRSSAAAKLRGQKRSGASGASAAPASAAAALAPSATRTRRSASQAGSKSQAVEKPP	60
Qy	61	SEKPRLRRSSPRAQEEGPGEPPELALLPPPPPPPTPATPTSSASNLDLGEQRRWET	120
Db	61	SEKPRLRRSSPRAQEEGPGEPPELALLPPPPPPPTPATPTSSASNLDLGEQRRWET	120
Qy	121	FQKRQKLTSEGAAKLLDTEFYQGLVKHTGGCHCGAVRFEVWASADLHIFDC	172
Db	121	FQKRQKLTSEGAAKLLDTEFYQGLVKHTGGCHCGAVRFEVWASADLHIFDC	172